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Wild animal rabies in India: Possibility of species spill over

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Background: Rabies is endemic in most parts of India, with the exception of Andaman and Nicobar and Lakshdweep islands and to some extent in Nagaland. In India, dogs play an important role in rabies transmission and maintenance, however very less is known about the role of wild animals in rabies transmission and maintenance. Phylogenetic analysis supports the evolution of lyssaviruses in bat vectors with occasional but regular spill over and host switching to carnivore vectors to extend the virus host range.

The present study is aimed at sequencing and phyloegnetic analysis of wild animal rabies virus isolates by targeting the nucleoprotein gene.

Methods & Materials: We collected 12 rabies suspected brain samples from different species of wild animals in India. The confirmatory diagnosis was made by direct fluorescent antibody test (dFAT) and nucleoprotien gene specific real time polymerase chain reaction (RT-PCR). The partial nucleoprotein gene was amplified and sequenced. The phylogenetic analysis was carried out with published N gene sequences from wild, domestic and human origin by DNAstar software.

Results: Eight out of twelve samples were found positive by dFAT and RT-PCR after run with specific controls. The partial N gene (803 bp) sequence analysis revealed the all rabies isolates were belonged to classical rabies virus of genotype 1 of rhabdovirus. These isolates were more closely related to other animal rabies virus isolates, indicating the spillover of species. Even though this event is rare, occasionally such an event can initiate a new virus-host relationship in which sustained propagation and independent transmission of the virus within the new host species occurs such that the new host species becomes a rabies reservoir. The full length nucleotide sequence analysis is also underway along with more number of samples to know precise virus type and the transmission of rabies virus from the reservoir host to the other host.

Conclusion: In conclusion the rabies virus isolates circulating in wild and domestic animals in India are more closely related genotypically and suggestive of species spill over.

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African tick bite fever in an immunosuppressed patient

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Background: African tick bite fever (AFBT) is an endemic zoonosis in certain parts of South Africa, transmitted by ticks. The incubation period is five to seven (up to ten) days. Symptoms may include fever, headaches, and at the bite site a black eschar. More than one simultaneously eschar may occur. We present a case of AFBT in an immunosuppressed patient with late progressively developing multiple eschars.

Methods & Materials: A 66 year old male with a medical history of rheumatoid arthritis on treatment with sulfasalazine and methotrexate was admitted with fever. Eleven days prior to admission two days were spend in the Kruger National Park, South Africa. At day two in the park he discovered a red mark on his right lower leg. Six days later now outside endemic area with all clothes washed and changed he felt malaise and feverish and many red marks developed on both legs and his left arm and continued to develop after returning home.

Results: On admission the patient presented with a temperature of 38.3 °C and multiple maculopapular, some pustular, elements of diameter 2 to 15 mm; 16 on his right leg; 10 on the left lower leg; one on the left arm. Within hospital stay the primary element with debut 12 days prior and surrounding elements developed into black eschars[1]. Blood works showed CRP of 60 mg/l (<8 mg/l), and normal sedimentation rate, liver enzymes, creatinine, electrolytes, leucocytes and haematology. Treatment was doxycycline 100 mg x 2 for seven days. Ten days later eight eschars had formed and multiple maculopopular elements persisted[2,3], and Rickettsia rickettsiii, spottet fever group IgM and IgG was positive.

Primary eschar, two black escars and one pustular element on second day of admission